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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/978,382A

DATE: 06/28/2002

TIME: 11:06:24

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Output Set: N:\CRF3\06282002\I978382A.raw

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3 <110> APPLICANT: Yanofsky, Martin F.
4   Liljegren, Sarah
5   The Regents of the University of California
7 <120> TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
8   Plants
10 <130> FILE REFERENCE: 19452A-000930US
12 <140> CURRENT APPLICATION NUMBER: US 09/978,382A
C--> 13 <141> CURRENT FILING DATE: 2002-06-18
15 <150> PRIOR APPLICATION NUMBER: US 60/090,649
16 <151> PRIOR FILING DATE: 1998-06-25
18 <150> PRIOR APPLICATION NUMBER: US 09/339,998
19 <151> PRIOR FILING DATE: 1999-06-25
21 <160> NUMBER OF SEQ ID NOS: 25
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28 <213> ORGANISM: Arabidopsis sp.
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40                                     1 5
42 gtt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163
43 Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe
44                                     10 15 20
46 tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211
47 Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val
48                                     25 30 35
50 ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259
51 Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys
52                                     40 45 50
54 ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307
55 Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg
56                                     55 60 65
58 tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355
59 Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val
60 70 75 80 85
62 tca caa agt gaa aat tgg gtt cta gaa cat gct aag ctc aag gca aga 403

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67 Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe Met Gly Glu Asp Leu
68          105          110          115
70 gat tcg ttg agc ttg aag gag ctc caa agc ttg gag cat cag ctc gat 499
71 Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu Glu His Gln Leu Asp
72          120          125          130
74 gca gct atc aag agc att agg tca aga aag aac caa gct atg ttc gaa 547
75 Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn Gln Ala Met Phe Glu
76          135          140          145
78 tcc ata tct gcg ctc cag aag aag gat aaa gcc ttg caa gat cac aac 595
79 Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala Leu Gln Asp His Asn
80 150          155          160          165
82 aat tcg ctt ctc aaa aag att aag gag agg gag aag aaa acg ggt cag 643
83 Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu Lys Lys Thr Gly Gln
84          170          175          180
86 caa gaa gga caa tta gtc caa tgc tcc aac tct tct tca gtt ctt ctg 691
87 Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser Ser Ser Val Leu Leu
88          185          190          195
90 cct caa tac tgc gta acc tcc tcc aga gat ggc ttt gtg gag aga gtt 739
91 Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly Phe Val Glu Arg Val
92          200          205          210
94 ggg gga gag aac ggt ggt gca tcg tcg ttg acg gaa cca aac tct ctg 787
95 Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr Glu Pro Asn Ser Leu
96          215          220          225
98 ctt ccg gct tgg atg tta cgt cct acc act acg aac gag tag 829
99 Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Thr Asn Glu
100 230          235          240
102 aactatctca ctctttataa tataatgata atataattaa tgtttaatat ttccataaca 889
104 ttcagcatttt ttttggtagc ttatactcat tattaatacc gatatgtttt agctagtcac 949
106 attatatgta tgatggaact ccgttgtaga gacgtatgta cgtaagctat cattagattc 1009
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121 His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe
122 35 40 45
123 Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu
124 50 55 60
125 Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu
126 65 70 75 80
127 Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala

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131 Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu
132          115          120          125
133 Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn
134          130          135          140
135 Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala
136 145          150          155          160
137 Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu
138          165          170          175
139 Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser
140          180          185          190
141 Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly
142          195          200          205
143 Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr
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157 <222> LOCATION: (7)..(753)
158 <223> OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
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163      1          5          10
165 aaa cta ggg aga ggg aaa ata gag ata aag agg ata gag aac aca aca 96
166 Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr
167 15          20          25          30
169 aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa 144
170 Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys
171          35          40          45
173 gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc 192
174 Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile
175          50          55          60
177 ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg 240
178 Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg
179          65          70          75
181 ggt aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct 288
182 Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro
183          80          85          90
185 cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct 336
186 Pro Ser Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser

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191          115          120          125
193 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432
194 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu
195          130          135          140
197 gaa gga cgt ctt gaa aaa gga atc agc cgt gtc cgc tcc aaa aag aat 480
198 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn
199          145          150          155
201 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528
202 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu
203          160          165          170
205 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576
206 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala
207 175          180          185          190
209 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624
210 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr
211          195          200          205
213 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672
214 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn
215          210          215          220
217 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720
218 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser
219          225          230          235
221 ggc caa gac caa cct cct ctt caa ctt gtg taa ctcaaaacat gataacttgt 773
222 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val
223          240          245
225 ttcttccct cataacgatt aagagagaga cgagagagtt catttttatat ttataacgcg 833
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241 20 25 30
242 Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr
243 35 40 45
244 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser
245 50 55 60
246 Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr
247 65 70 75 80
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251          100          105          110
252 Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly
253          115          120          125
254 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly
255          130          135          140
256 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu
257 145          150          155          160
258 Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu Leu Gln
259          165          170          175
260 His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala Arg Leu
261          180          185          190
262 Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr
263          195          200          205
264 Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn
265          210          215          220
266 Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser Gly Gln
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268 Asp Gln Pro Pro Leu Gln Leu Val
269          245
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273 <211> LENGTH: 959
274 <212> TYPE: DNA
275 <213> ORGANISM: Arabidopsis sp.
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278 <221> NAME/KEY: CDS
279 <222> LOCATION: (78)..(818)
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286          Met Glu Gly Gly Ala Ser Asn Glu Val Ala Glu
287          1          5          10
289 agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag 158
290 Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu
291          15          20          25
293 aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta 206
294 Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu
295          30          35          40
297 ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct 254
298 Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala
299          45          50          55
301 ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac 302
302 Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn
303 60          65          70          75
305 agt gtg aga gga aca ata gaa agg tac aag aaa gct tgc tcc gac gcc 350
306 Ser Val Arg Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala
307          80          85          90
309 gtt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398
310 Val Asn Pro Pro Thr Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln

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VERIFICATION SUMMARY

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